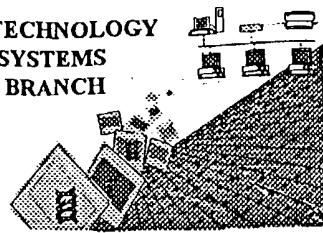# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: /0/005,228A
Source: 1Fwi/6
Date Processed by STIC: 10/4/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
   U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/005,228A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics
___ Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

·2 ___ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
___ Numbering   use space characters, instead.

4 ___ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ___ Variable Length   Sequence(s)___contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ___ PatentIn 2.0
___ "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ___ Skipped Sequences
___ (OLD RULES)
Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ___ Skipped Sequences
___ (NEW RULES)
Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's
___ (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ___ Invalid <213>
___ Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence.

11 ___ Use of <220>   Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0
___ "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n/Xaa   "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

IFW16

```
RAW SEQUENCE LISTING            DATE: 10/04/2004
PATENT APPLICATION:  US/10/005,228A   TIME: 10:43:11

     Input Set : A:\PTO.LM.txt
     Output Set: N:\CRF4\10042004\J005228A.raw
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 3 <110> APPLICANT: Genetics Institute
 4        Karen, Lyons
 5        Vicki, Rosen
 6        Aaron, Daluiski
 7        Thomas, Engstrand
 8        Matthew, Bahamonde
 9        Gamer, Laura
10        Agius, Eric
12 <120> TITLE OF INVENTION: Method and Composition for Modulating Bone Growth
14 <130> FILE REFERENCE: 22058-554 UTIL
16 <140> CURRENT APPLICATION NUMBER: 10/005,228A
17 <141> CURRENT FILING DATE: 2001-12-03
19 <150> PRIOR APPLICATION NUMBER: US 60/250,535
20 <151> PRIOR FILING DATE: 2000-12-01
22 <160> NUMBER OF SEQ ID NOS: 9
24 <170> SOFTWARE: PatentIn version 3.2
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ERRORED SEQUENCES

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      27 <211> LENGTH: 2952
      28 <212> TYPE: DNA
      29 <213> ORGANISM: Homo sapiens
      31 <400> SEQUENCE: 1
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E--> 35 ctgtaatgca gtgctgtgac catagcccac tgcagcctcc acctcccagg ctcaagcagt
     36 120
E--> 38 ccttcccccc tcgccctcat gaatagctgg gactacagcc tggagcattg gtaagcgtca
     39 180
E--> 41 cactgccaaa gtgagagctg ctggagaact cataatccca ggaacgcctc ttctactctc
     42 240
E--> 44 cgagtacccc agtgaccaga gtgagagaag ctctgaacga gggcacgcgg cttgaaggac
     45 300
E--> 47 tgtgggcaga tgtgaccaag agcctgcatt aagttgtaca atggtagatg gagtgatgat
     48 360
E--> 50 tcttcctgtg cttatcatga ttgctctccc ctcccctagt atggaagatg agaagcccaa
     51 420
E--> 53 ggtcaacccc aaactctaca tgtgtgtgtg tgaaggtctc tcctgcggta atgaggacca
     54 480
E--> 56 ctgtgaaggc cagcagtgct tttcctcact gagcatcaac gatggcttcc acgtctacca
     57 540
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     60 600
E--> 62 tggccaagct gtggagtgct gccaggggga ctggtgtaac aggaacatca cggcccagct
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E--> 65 gcccactaaa ggaaaatcct tccctggaac acagaatttc cacttggagg ttggcctcat
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     69 780
E--> 71 aaaatttaaa aggcgcaacc aagaacgcct caatccccga gacgtggagt atggcactat
     72 840
E--> 74 cgaagggctc atcaccacca atgttggaga cagcacttta gcagatttat tggatcattc
     75 900
E--> 77 gtgtacatca ggaagtggct ctggtcttcc ttttctggta caaagaacag tggctcgcca
     78 960
E--> 80 gattacactg ttggagtgtg tcgggaaagg caggtatggt gaggtgtgga ggggcagctg
     81 1020
E--> 83 gcaaggggaa aatgttgccg tgaagatctt ctcctcccgt gatgagaagt catggttcag
     84 1080
E--> 86 ggaaacggaa ttgtacaaca ctgtgatgct gaggcatgaa aatatcttag gtttcattgc
     87 1140
E--> 89 ttcagacatg acatcaagac actccagtac ccagctgtgg ttaattacac attatcatga
     90 1200
E--> 92 aatgggatcg ttgtacgact atcttcagct tactactctg gatacagtta gctgccttcg
     93 1260
E--> 95 aatagtgctg tccatagcta gtggtcttgc acatttgcac atagagatat ttgggaccca
     96 1320
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     99 1380
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     117 1740
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     120 1800
E--> 122 agcactgcgt atcaaaaaga ctttgaccaa aattgataat tccctcgaca aattgaaaac
     123 1860
E--> 125 tgactgttga cattttcata gtgtcaagaa ggaagatttg acgttgttgt cattgtccag
     126 1920
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     129 1980
E--> 131 aatggctgct ttgacaaggc agacgtcgta cccagccatg tgttggggag acatcaaaac
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same error

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/005,228A

DATE: 10/04/2004
TIME: 10:43:11

Input Set : **A:\PTO.LM.txt**
Output Set: **N:\CRF4\10042004\J005228A.raw**

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E--> 134 caccctaacc tcgctcgatg actgtgaact gggcatttca cgaactgttc acactgcaga
       135 2100
E--> 137 gactaatgtt ggacagacac tgttgcaaag gtagggactg gaggaacaca gagaaatcct
       138 2160
E--> 140 aaaagagatc tgggcattaa gtcagtggct ttgcatagct ttcacaagtc tcctagacac
       141 2220
E--> 143 tccccacggg aaactcaagg aggtggtgaa tttttaatca gcaatattgc ctgtgcttct
       144 2280
E--> 146 cttctttatt gcactaggaa ttctttgcat tccttacttg cactgttact cttaatttta
       147 2340
E--> 149 aagacccaac ttgccaaaat gttggctgcg tactccactg gtctgtcttt ggataatagg
       150 2400
E--> 152 aattcaattt ggcaaaacaa aatgtaatgt cagactttgc tgcattttac acatgtgctg
       153 2460
E--> 155 atgtttacaa tgatgccgaa cattaggaat tgtttataca caactttgca aattatttat
       156 2520
E--> 158 tacttgtgca cttagtagtt tttacaaaac tgctttgtgc atatgttaaa gcttattttt
       159 2580
E--> 161 atgtggtctt atgattttat tacagaaatg tttttaacac tatactctaa aatggacatt
       162 2640
E--> 164 ttcttttatt atcagttaaa atcacatttt aagtgcttca catttgtatg tgtgtagact
       165 2700
E--> 167 gtaacttttt ttcagttcat atgcagaacg tatttagcca ttacccacgt gacaccaccg
       168 2760
E--> 170 aatatattat cgatttagaa gcaaagattt cagtagaatt ttagtcctga acgctacggg
       171 2820
E--> 173 gaaaatgcat tttcttcaga attatccatt acgtgcattt aaactctgcc agaaaaaaat
       174 2880
E--> 176 aactattttg ttttaatcta ctttttgtat ttagtagtta tttgtataaa ttaaataaac
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       180 2952
       318 <210> SEQ ID NO: 3
       319 <211> LENGTH: 1969
       320 <212> TYPE: DNA
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       328 120
E--> 330 gagcgagccc ctccccggct ccagcccggt ccggggccgc gccggacccc agcccgccgt
       331 180
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E--> 336 aggctagcgc cccgccaccc gcagagcggg cccagaggga ccatgacctt gggctccccc
       337 300
E--> 339 aggaaaggcc ttctgatgct gctgatggcc ttggtgaccc agggagaccc tgtgaagccg
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```
       340  360
E--> 342 tctcggggcc cgctggtgac ctgcacgtgt gagagcccac attgcaaggg gcctacctgc
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E--> 345 cggggggcct ggtgcacagt agtgctggtg cgggaggagg ggaggcaccc ccaggaacat
       346  480
E--> 348 cggggctgcg ggaacttgca cagggagctc tgcagggggc gccccaccga gttcgtcaac
       349  540
E--> 351 cactactgct gcgacagcca cctctgcaac cacaacgtgt ccctggtgct ggaggccacc
       352  600
E--> 354 caacctcctt cggagcagcc gggaacagat ggccagctgg ccctgatcct gggccccgtg
       355  660
E--> 357 ctggccttgc tggccctggt ggccctgggt gtcctgggcc tgtggcatgt ccgacggagg
       358  720
E--> 360 caggagaagc agcgtggcct gcacagcgag ctgggagagt ccagtctcat cctgaaagca
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       370  960
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       373  1020
E--> 375 aacacagtat tgctcagaca cgacaacatc ctaggcttca tcgcctcaga catgacctcc
       376  1080
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       385  1260
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       388  1320
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       406  1680
E--> 408 tgatgcggga gtgctggtac ccaaacccct ctgcccgact caccgcgctg cggatcaaga
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       412  1800
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RAW SEQUENCE LISTING   DATE: 10/04/2004
PATENT APPLICATION: US/10/005,228A   TIME: 10:43:11

Input Set : A:\PTO.LM.txt
Output Set: N:\CRF4\10042004\J005228A.raw

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--> 414 gcacctgatt cctttctgcc tgcaggggge tggggggggtg gggggcagtg gatggtgccc
    415 1860
--> 417 tatctgggta gaggtagtgt gagtgtggtg tgtgctgggg atgggcagct gcgcctgcct
    418 1920
:--> 420 gctcggcccc cagcccaccc agccaaaaat acagctgggc tgaaacctg
    421 1969
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    574 <211> LENGTH: 1774
    575 <212> TYPE: DNA
    576 <213> ORGANISM: Homo sapiens
    578 <400> SEQUENCE: 6
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    580 60
:--> 582 gtggagacgg cgcccgcagc gccctgcgcg ggtgaggtcc gcgcagctgc tggggaagag
    583 120
:--> 585 cccacctgtc aggctgcgct gggtcagcgc agcaagtggg gctggccgct atctcgctgc
    586 180
:--> 588 acccggccgc gtcccgggct ccgtgcgccc tcgccccagc tggtttggag ttcaaccctc
    589 240
:--> 591 ggctccgccg ccggctcctt gcgccttcgg agtgtcccgc agcgacgccg ggagccgacg
    592 300
:--> 594 cgccgcgcgg gtacctagcc atggctgggg cgagcaggct gctctttctg tggctgggct
    595 360
:--> 597 gcttctgcgt gagcctggcg cagggagaga gaccgaagcc acctttcccg gagctccgca
    598 420
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    601 480
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    604 540
:--> 606 ggacaccggg ctccctggag ggaggctcgc agccctggcg ccctcggctc ctgcgcgaag
    607 600
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    613 720
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    625 960
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:--> 633 gtgtggtatc aagcttacag ggacaccgga attttcccac tggaactgtt cccaaatggg
    634 1140
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     637 1200
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     640 1260
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     643 1320
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     646 1380
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     652 1500
E--> 654 ttgatgccta ttattgctct ggagcatgcc agttccccat gccaaagtct ttgaagccat
     655 1560
E--> 657 caaatcatgc taccatccag agtatagtga gagctgtggg ggtcgttcct gggattcctg
     658 1620
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     661 1680
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     798 <211> LENGTH: 17
     799 <212> TYPE: DNA
     800 <213> ORGANISM: Artificial Sequence
     802 <220> FEATURE:
     803 <223> OTHER INFORMATION: Description of Artificial Sequence: RT-PCR Primer
     805 <400> SEQUENCE: 8
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     807 17
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     815 <220> FEATURE:
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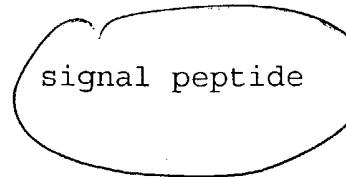<210>   5
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<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence: (signal peptide) give
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of genetic
material
in <2237
response

(see item 11
on Error Summary
Sheet)

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L:41 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:240 SEQ:1
L:44 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:300 SEQ:1
L:47 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:360 SEQ:1
L:50 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:420 SEQ:1
L:53 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:480 SEQ:1
L:56 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:540 SEQ:1
L:59 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:600 SEQ:1
L:62 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:660 SEQ:1
L:65 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:720 SEQ:1
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L:77 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:960 SEQ:1
L:80 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1020 SEQ:1
L:83 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1080 SEQ:1
L:86 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1140 SEQ:1
L:89 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1200 SEQ:1
L:92 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1260 SEQ:1
L:95 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1320 SEQ:1
L:98 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1380 SEQ:1
L:101 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1440 SEQ:1
L:104 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1500 SEQ:1
L:107 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1560 SEQ:1
L:110 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1620 SEQ:1
L:113 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1680 SEQ:1
L:116 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1740 SEQ:1
L:119 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1800 SEQ:1
L:122 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1860 SEQ:1
L:125 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1920 SEQ:1
L:128 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1980 SEQ:1
L:131 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:2040 SEQ:1
L:134 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:2100 SEQ:1
L:137 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:2160 SEQ:1
L:140 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:2220 SEQ:1
L:143 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:2280 SEQ:1
L:146 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:2340 SEQ:1
L:149 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:2400 SEQ:1
L:152 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:2460 SEQ:1
L:155 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:2520 SEQ:1
L:158 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:2580 SEQ:1
L:161 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:2640 SEQ:1
L:164 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:2700 SEQ:1
L:167 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:2760 SEQ:1
L:170 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:2820 SEQ:1
L:173 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:2880 SEQ:1
```

Input Set : **A:\PTO.LM.txt**
Output Set: **N:\CRF4\10042004\J005228A.raw**

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L:176 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:2940 SEQ:1
L:179 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:2952 SEQ:1
L:324 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:3
L:327 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:120 SEQ:3
L:330 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:180 SEQ:3
L:333 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:240 SEQ:3
L:336 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:300 SEQ:3
L:339 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:360 SEQ:3
L:342 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:420 SEQ:3
L:345 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:480 SEQ:3
L:348 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:540 SEQ:3
L:351 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:600 SEQ:3
L:354 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:660 SEQ:3
L:357 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:720 SEQ:3
L:360 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:780 SEQ:3
L:363 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:840 SEQ:3
L:366 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:900 SEQ:3
L:369 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:960 SEQ:3
L:372 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1020 SEQ:3
L:375 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1080 SEQ:3
L:378 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1140 SEQ:3
L:381 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1200 SEQ:3
L:384 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1260 SEQ:3
L:387 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1320 SEQ:3
L:390 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1380 SEQ:3
L:393 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1440 SEQ:3
L:396 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1500 SEQ:3
L:399 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1560 SEQ:3
L:402 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1620 SEQ:3
L:405 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1680 SEQ:3
L:408 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1740 SEQ:3
L:411 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1800 SEQ:3
L:414 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1860 SEQ:3
L:417 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1920 SEQ:3
L:420 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1969 SEQ:3
L:579 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:6
L:582 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:120 SEQ:6
L:585 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:180 SEQ:6
L:588 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:240 SEQ:6
L:591 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:300 SEQ:6
L:594 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:360 SEQ:6
L:597 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:420 SEQ:6
L:600 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:480 SEQ:6
L:603 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:540 SEQ:6
L:606 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:600 SEQ:6
L:609 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:660 SEQ:6
L:612 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:720 SEQ:6
L:615 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:780 SEQ:6
L:618 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:840 SEQ:6
```

Input Set : **A:\PTO.LM.txt**
Output Set: **N:\CRF4\10042004\J005228A.raw**

```
L:621 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:900 SEQ:6
L:624 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:960 SEQ:6
L:627 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1020 SEQ:6
L:630 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1080 SEQ:6
L:633 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1140 SEQ:6
L:636 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1200 SEQ:6
L:639 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1260 SEQ:6
L:642 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1320 SEQ:6
L:645 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1380 SEQ:6
L:648 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1440 SEQ:6
L:651 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1500 SEQ:6
L:654 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1560 SEQ:6
L:657 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1620 SEQ:6
L:660 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1680 SEQ:6
L:663 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1740 SEQ:6
L:666 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1774 SEQ:6
L:806 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:17 SEQ:8
L:819 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:17 SEQ:9
L:825 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:827 M:254 E: No. of Bases conflict, this line has no nucleotides.
```